

Figure 3

SEQ ID NO: 5

aaataataat ataaatttag ttttaagtaa aaacttcgga aaaaaatgtg acttcgcttg  
 60 aaatgcgaa ggtgtcttt cgaagaagca gctatttcca atattctgc cttttgaaa  
 120 gtcgagaaca agaattaatc ttttttcgac tttatttcat cattatttag gatagttctt  
 180 atg ttg aat aaa gca ggc att gca gag ccg agc ttg ttg act cgt gcg  
 228 Met Leu Asn Lys Ala Gly Ile Ala Glu Pro Ser Leu Trp Thr Arg Ala  
 1 5 10 15  
 gat gct atg aaa gtg cat acc gat gat ccc acg gca acc atg cct acc  
 276 Asp Ala Met Lys Val His Thr Asp Asp Pro Thr Ala Thr Met Pro Thr  
 20 25 30  
 att gat tat gac ttt cct gtc atg act gat aaa tat tgg gtt tgg gac  
 324 Ile Asp Tyr Asp Phe Pro Val Met Thr Asp Lys Tyr Trp Val Trp Asp  
 35 40 45  
 act tgg ccc tta cgc gat att aac ggt cag gtt gtc agc ttc caa ggt  
 372 Thr Trp Pro Leu Arg Asp Ile Asn Gly Gln Val Val Ser Phe Gln Gly  
 50 55 60  
 tgg tcg gtg atc ttt gct ttg gtc gct gat cgc acc aaa tat ggt tgg  
 420 Trp Ser Val Ile Phe Ala Leu Val Ala Asp Arg Thr Lys Tyr Gly Trp  
 65 70 75  
 cat aat cgc aat gat ggc gcc aga att ggt tat ttc tat tca cgt ggt  
 468 His Asn Arg Asn Asp Gly Ala Arg Ile Gly Tyr Phe Tyr Ser Arg Gly  
 80 85 90  
 gga agc aac tgg att ttt ggt ggt cat ctt ctg aaa gat ggt gcc aat  
 516 Gly Ser Asn Trp Ile Phe Gly Gly His Leu Leu Lys Asp Gly Ala Asn  
 100 105 110  
 ccg cgt tct tgg gaa tgg tct ggt tgc acg att atg gca ccg ggt acg  
 564 Pro Arg Ser Trp Glu Trp Ser Gly Cys Thr Ile Met Ala Pro Gly Thr  
 115 120 125  
 gcc aat tct gtc gaa gta ttc ttt acg tct gtc aat gat acg ccg tca  
 612 Ala Asn Ser Val Glu Val Phe Phe Thr Ser Val Asn Asp Thr Pro Ser  
 130 135 140  
 gaa tcc gtt cct gcc cag tgc aag ggc tac atc tat gcc gat gat aaa  
 660 Glu Ser Val Pro Ala Gln Cys Lys Gly Tyr Ile Tyr Ala Asp Asp Lys  
 145 150 155  
 tcg gta tgg ttt gac ggt ttt gat aaa gtc acc gat ctg ttt cag gca  
 708 Ser Val Trp Phe Asp Gly Phe Asp Lys Val Thr Asp Leu Phe Gln Ala  
 165 170 175  
 gat ggc ctt tat tat gct gat tat gca gaa aat aat ttc tgg gat ttc  
 756 Asp Gly Leu Tyr Trp Tyr Ala Asp Tyr Ala Glu Asn Asn Phe Trp Asp Phe  
 180 185 190  
 cgc gat ccg cat gtc ttc att acc ccg aag ata ggc aaa aca tat gcc  
 804 Arg Asp Pro His Val Phe Ile Thr Pro Lys Ile Gly Lys Thr Tyr Ala  
 195 200 205  
 ttg ttt gaa ggt aat gtt gcc atg gag cgc ggt acg gtc gct gtt ggc  
 852 Leu Phe Glu Gly Asn Val Ala Met Glu Arg Gly Thr Val Ala Val Gly  
 210 215 220  
 gaa gag gaa att ggc cct gtt cca cca aaa acc gaa acc gct gat ggc  
 900 Glu Glu Glu Ile Gly Pro Val Pro Lys Thr Glu Thr Pro Asp Gly  
 225 230 235  
 gct cgc tat tgt gct gct gcc att ggt att gca cag gcc ctt aat gaa  
 948 Ala Arg Tyr Cys Ala Ala Ala Ile Gly Ile Ala Gln Ala Leu Asn Glu  
 245 250 255  
 gcc cgc acc gaa tgg aaa ttg tta ccg cct ttg gta acc gcc ttt ggt  
 996 Ala Arg Thr Glu Trp Lys Leu Leu Pro Pro Leu Val Thr Ala Phe Gly  
 260 265 270  
 gtc aat gac cag acg gag ccg cct cat gtc gtt ttc cag aat ggc ttg  
 1044 Val Asn Asp Gln Thr Glu Arg Pro His Val Val Phe Gln Asn Gly Leu  
 275 280 285  
 acc tat ctc ttt acg atc agt cat cat tgc act tat gcc gat ggt ttg  
 1092 Thr Tyr Leu Phe Thr Ile Ser His His Ser Thr Tyr Ala Asp Gly Leu  
 290 295 300  
 tcg ggt cct gat ggg gtt tat ggc ttt gtt tct gaa aac ggc att ttt  
 1140 Ser Gly Pro Asp Gly Val Tyr Phe Val Ser Glu Asn Gly Ile Phe  
 305 310 315  
 ggc cct tat gaa ccg ctg aat ggt tcc ggt ttg gtt ctc ggt aac ccg  
 1188 Gly Pro Tyr Glu Pro Leu Asn Gly Ser Gly Leu Val Leu Gly Asn Pro  
 325 330 335  
 tct tca cag cct gat cag gct tat tcc cat tat gtc atg aca aat ggc  
 1236 Ser Ser Gln Pro Tyr Gln Ala Tyr Ser His Tyr Val Met Thr Asn Gly  
 340 345 350  
 ctg gtg acc tcc ttc att gat acc att ccg agt tct gac ccg aat gtc  
 1284 Leu Val Thr Ser Phe Ile Asp Thr Ile Pro Ser Ser Asp Pro Asn Val  
 355 360 365  
 tat cgt tat ggt ggc acc ttg gca ccg acc atc aaa ttg gaa ttg gtt  
 1332 Tyr Arg Tyr Gly Gly Thr Leu Ala Pro Thr Ile Lys Leu Glu Leu Val  
 370 375 380  
 ggc cat cgc agc ttc gtt acc gaa gaa ggt aag ggt tat gcc tat att ccg  
 1380 Gly His Arg Ser Phe Val Thr Glu Val Lys Gly Tyr Tyr Ile Pro  
 385 390 395  
 cca cag atc gag tgg ttg gca gaa gat gaa tct tct aat tct gcg gca  
 1428 Pro Gln Ile Glu Trp Leu Ala Glu Asp Glu Ser Ser Asn Ser Ala Ala  
 405 410 415  
 gcc ctg tct tta ttg aat aaa taagatttat tcattgtaaa tgaactttct  
 1479 Ala Leu Ser Leu Leu Asn Lys  
 420  
 gattatgctt gaataaagca ttatcatctt ttgagtttat ttoacttaa ggtcatcag  
 1539 ggcattttgc cctgagaca ccttctctat tcttaataat aatticaaga aagtgatat  
 1599 tactttaaat gtttaatttt aatgcagtc gctggacgc agcccaagcg atgaagtga  
 1659 ataaatttga ttgacgacc tctatgcgg aaatcggac tgattttccc attatgcgtg  
 1719 atgactttg gctgtggat acttggccat tacgggatat caatggcaat cctgtcagct  
 1779 ttaaggctg gaatgtatt t